

		Domain Ia									
		A ₀	B ₀	C ₀	D ₀						
TBEV E	281	SRCHLENRD	FVTGTGQTR	VTLVLEGGC	VTTIA-EGKP--S	MDV-WLDAIQ	E	-----	-----	-----	-----
HCV E1	192				Y QVRNSSLGH VTNDG	-----FNSS	VYERADAILH	-----	-----	-----	-----
CSFV E2	689				GQLACK	EDRYAISST	NEIGLLGAGG	LATTWKEYNDLQL	NDGTVKICVAG	SPKVTALNVV	SRRYVLA
		FUSION PEPTIDE									
		Domain IIa									
		a	b	c	d	e					
TBEV E	332	NP---AKTREY---	CL HAKLSDTKVA	ARCPMTGPAF	LAEEHQGGTV	CRDQSDRGW	Q--NHCGL-FKKG	SIYACVKRAAC	EAKKKATGHV	YDAN	
HCV E1	223	TPGCVPCVREGNASRCW	VA-VTPT-VA	TRGK-L-PTT	-----Q---	L RRHIDLWGS	A--TLCSALTV-Q	DL--CGSVFL	VGQLFTFSFR	HHWT	
CSFV E2	757	SLHKKALPISVTFELLE	DGTNFTSEEM	EDDFGFLCP	FDTSFVVKGK	YNTT-LINGS	AFYLVCPIGW-TG	VI-ECTAV--	SP--TTL--R	TEVV	
		Domain IIb									
		F ₀	G ₀	H ₀							
TBEV E	416	KIVTVKVED	ETGDYVAANE	THSGKRTAGF	TISSEKILT	MGEGDVSL	CRVASGVDL	-----	-----	-----	-----
HCV E1	---	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
CSFV E2	---	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
		Domain IIB									
		f	g	h	i	j	k	l			
TBEV E	475	AQVILELDK	TVEHLPTAQ	VHR-CWENDLA	LPWKHEGAQN	WNNARLVEF	GAPHAVKMDV	YNLGDQTVL	LKALAGVFA	-HIEGKXHL	KS
HCV E1	301	-----TQDC	NCSIYPGHIT	CHRMAN-NMM	N-MSPTAAL-	-----VVAQLL	RIFQAI-MDM	I-AGAHMGVL	-----AGI-	-----K	---
CSFV E2	842	-----K	TF--RRDKPF	PHRMDCVTTTV	ENEDLFYCKL	GGNWTGVK--	GEP-VVYTG	V-Y-KQCRWC	GPDENEPLGL	PHYPIGK	---

Figure 1A



Figure 1A cont.

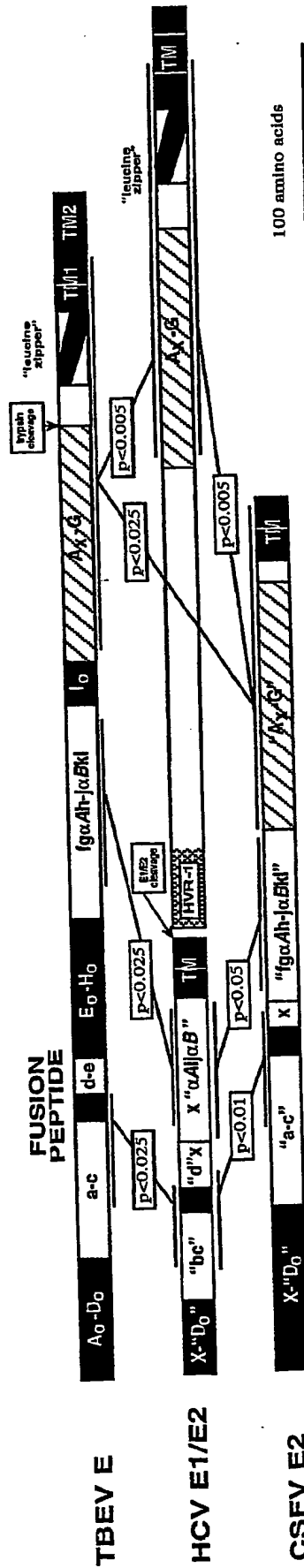


Figure 1B

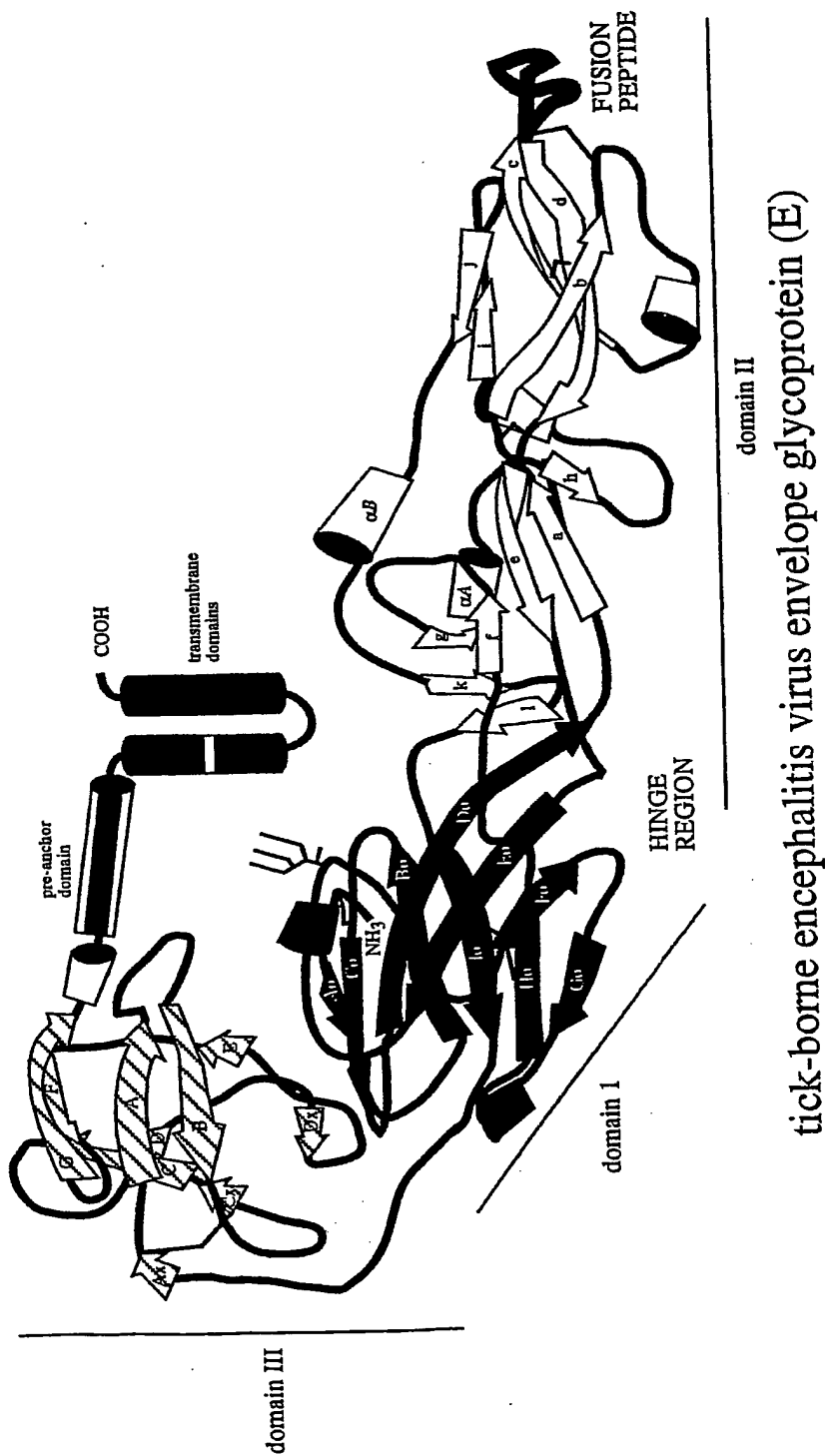
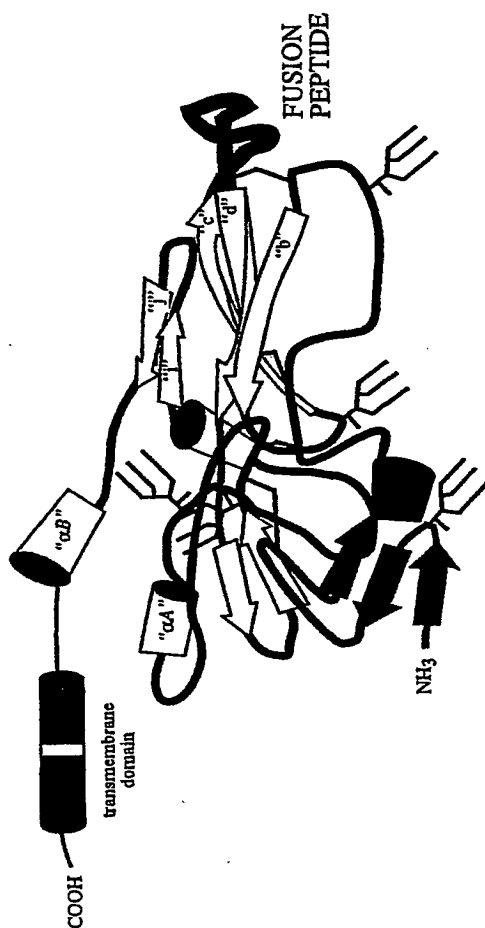


Figure 2



hepatitis C virus envelope glycoprotein 1 (E1)

Figure 2 cont.



classic swine fever virus envelope glycoprotein 2 (E2)

Figure 2 cont.

A

TBEV prM	72	TLAATVRKER DGSTVIRAEG KDAATQVRVE NGTCVI--LATD MGSWCDDSL
CSFV E1	491	LSPYCN VTSKIGYIWTY TNNCTPACLP KN-TKIIGPG KFDNAEDGK ILHENGHLS-E FLLLSLVVLS
TBEV prM	164	-----YECVTIDQG-E EPVDVDCFCR NVDGVYLEYG RCGKQEGSRT RRSVLIPSHA-
CSFV E1	561	DFAPETASAL YLIFHYV-IPQSHE EPEGCDTNQL NLT-VEL---RTEDVIPSSVW
TBEV prM	214	-QGELTGRGHK WLEGDSLRTH LTRVEGWVWK NKLLALAMVT VVWLTLESVV
CSFV E1	611	NVGKVVCVRPD WWPYETKVAL LPEEAGQVVK LALRALRDLT RVW---NSAS
TBEV prM	264	TRVAVLVVLL CLAPVYA
CSFV E1	659	TT----AFLI CLIKVLRGQIVQGVIM LLLVTGAQ

B

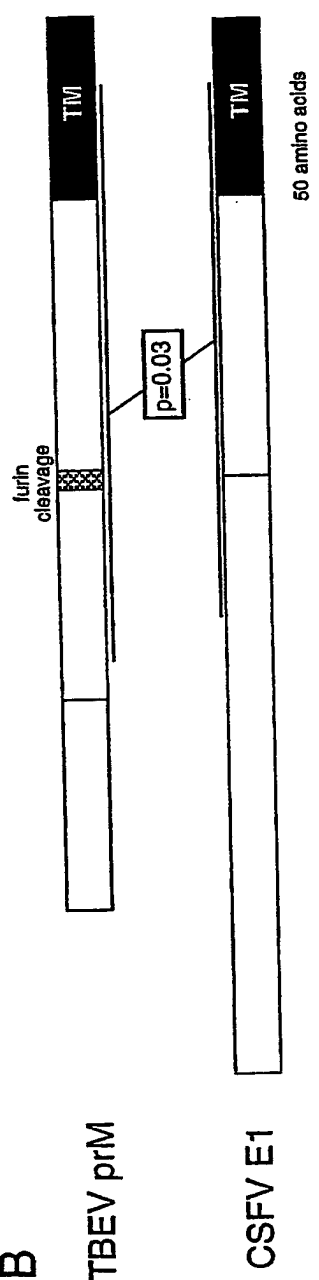


Figure 3

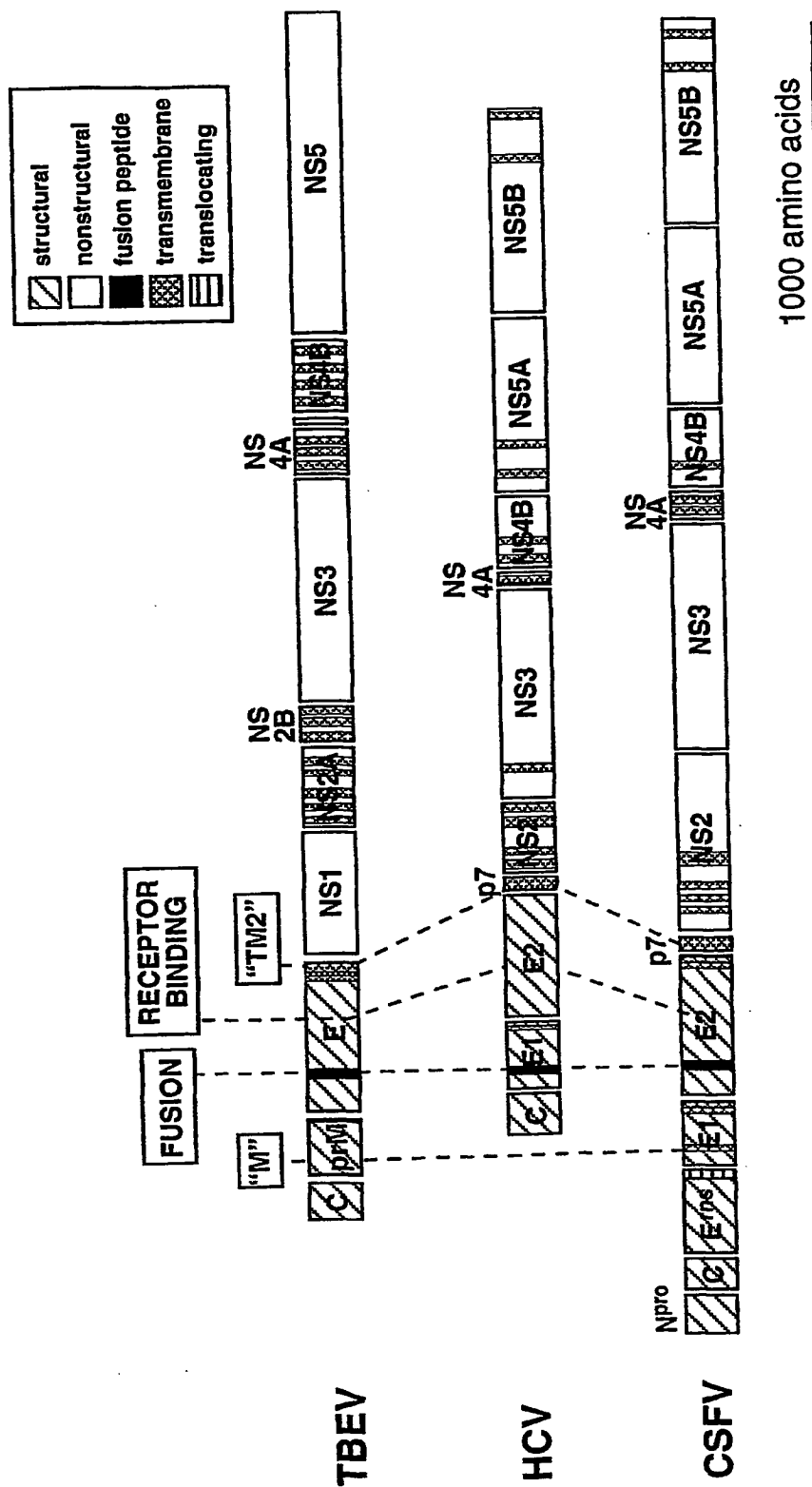


Figure 4

Figure 5

